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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 17.0123 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-1

Perfect score: 83

Sequence: 1 KHKHKHKGKHKHK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6 COMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	Score	Query Match	Length	DB	ID	Description
1	68	84.0	1199	2	US-09-208-742-2	Sequence 2, Appli
2	68	84.0	1199	2	US-09-332-295-4	Sequence 4, Appli
3	68	84.0	1199	2	US-09-709-979-4	Sequence 4, Appli
4	68	84.0	1199	. 2	US-10-147-268-4	Sequence 4, Appli
5	64.5	79.6	224	2	US-09-902-540-12716	Sequence 12716, A
6	57	70.4	297	2	US-09-248-796A-22393	Sequence 22393, A
7	56	69.1	1213	1	US-08-188-582-20	Sequence 20, Appl
8	56	69.1	1213	1	US-08-646-715-20	Sequence 20, Appl
9	55	67.9	10	2	US-10-104-307-18	Sequence 18, Appl
10	53	65.4	18	1	US-08-346-849-64	Sequence 64, Appl
11	53	65.4	18	1	US-08-293-284A-64	Sequence 64, Appl
12	53	65.4	18	2	US-08-898-300-64	Sequence 64, Appl
13	53	65.4	18	2	US-08-824-513-64	Sequence 64, Appl
14	53	65.4	313	2	US-08-686-528A-3	Sequence 3, Appli
15	53	65.4	313	2	US-09-456-287-3	Sequence 3, Appli
16	53	.65.4	337	2	US-08-686-528A-2	Sequence 2, Appli
17	53	65.4	337	2	US-09-456-287-2	Sequence 2, Appli
18	51.5	63.6	28	2	US-09-437-912-6	Sequence 6, Appli
19	51.5	63.6	47	2	US-09-612-126-4	Sequence 4, Appli
20	51.5	63.6	62	2	US-09-612-126-7	Sequence 7, Appli
21	51.5	63.6	83	2	US-09-612-126-6	Sequence 6, Appli

22	51.5	63.6	94	2	US-09-612-126-10	Coguence 10 Anni
						Sequence 10, Appl
23	51.5	63.6	179	2	US-09-612-126-11	Sequence 11, Appl
24	51.5	63.6	186	2	US-09-612-126-8	Sequence 8, Appli
25	51.5	63.6	255	2	US-09-612-126-1	Sequence 1, Appli
26	51.5	63.6	255	2	US-10-129-946-1	Sequence 1, Appli
27	51.5	63.6	415	3	US-10-162-335-76	Sequence 76, Appl
28	51.5	63.6	579	2	US-09-949-002-475	Sequence 475, App
29	51.5	63.6	579	2	US-09-949-002-481	Sequence 481, App
30	51.5	63.6	615	3		
					US-10-162-335-72	Sequence 72, Appl
31	51.5	63.6	644	3	US-10-162-335-74	Sequence 74, Appl
32	51.5	63.6	. 644	3	US-10-162-335-84	Sequence 84, Appl
33	50	61.7	110	2	US-09-513-999C-7836	Sequence 7836, Ap
34	50	61.7	381	2	US-09-919-497-96	
						Sequence 96, Appl
35	49.5	61.1	55	2	US-09-270-767-61691	Sequence 61691, A
36	49.5	61.1	199	2	US-09-270-767-46135	Sequence 46135, A
37	49	60.5	14	2	US-09-648-569A-42	Sequence 42, Appl
38	49	60.5	14	2	US-09-904-196B-12	
						Sequence 12, Appl
39	49	60.5	14	2	US-09-760-008A-12	Sequence 12, Appl
40	49	60.5	14	2	US-09-782-587B-15	Sequence 15, Appl
41	49	60.5	14	2	US-10-192-294-12	Sequence 12, Appl
42	49	60.5	14	2	US-09-997-623-44	
						Sequence 44, Appl
43	49	60.5	14	2	US-10-195-707B-38	Sequence 38, Appl
44	49	60.5	14	3	US-09-806-703A-24	Sequence 24, Appl
45	49	60.5	15	2	US-09-904-196B-5	Sequence 5, Appli
46	49	60.5	15	2	US-09-760-008A-5	Sequence 5, Appli
						=
47	49	60.5	15	2	US-09-556-818-26	Sequence 26, Appl
48	49	60.5	15	2	US-09-782-587B-16	Sequence 16, Appl
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50	49	60.5	15	2	US-09-997-623-45	Sequence 45, Appl
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52	49	60.5	173	2	US-09-396-937-12	Sequence 12, Appl
53	49	60.5	173	2	US-09-396-937-18	Sequence 18, Appl
54	49	60.5	173	2	US-09-396-937-20	Sequence 20, Appl
55	49	60.5	182	2	US-09-396-937-16	
						Sequence 16, Appl
56	49	60.5	187	2	US-09-396-937-8	Sequence 8, Appli
57	49	60.5	188	2	US-09-396-937-14	Sequence 14, Appl
58	48.5	59.9	300	2	US-09-395-689-1	Sequence 1, Appli
59	48.5	59.9	765	1	US-08-663-112-2	Sequence 2, Appli
60	48.5	59.9	765	2	US-09-538-092-906	
						Sequence 906, App
61	48.5	59.9	765	2	US-09-882-274-2	Sequence 2, Appli
62	48	59.3	582	2	US-09-976-594-733	Sequence 733, App
63	48	59.3	1097	3	US-08-951-188A-4	Sequence 4, Appli
64	47	58.0	213	2	US-09-252-991A-17343	Sequence 17343, A
65	47					
		58.0	218	2	US-09-252-991A-25291	Sequence 25291, A
66	47	58.0	1716	2	US-09-949-016-11331	Sequence 11331, A
67	46	56.8	117	2	US-09-513-999C-5282	Sequence 5282, Ap
68	46	56.8	363	2	US-10-094-749-1983	Sequence 1983, Ap
69	46	56.8	425	2	US-09-270-767-45380	
						Sequence 45380, A
70	46	56.8	618	2	US-09-248-796A-14560	Sequence 14560, A
71	46	56.8	713	2	US-09-252-991A-19477	Sequence 19477, A
72	45.5	56.2	531	2	US-09-270-767-32631	Sequence 32631, A
73	45.5	56.2	531	2	US-09-270-767-47848	Sequence 47848, A
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			16		US-08-346-849-49	Sequence 49, Appl
75	45	55.6	16	1	US-08-293-284A-49	Sequence 49, Appl
76	45	55.6	16	2	US-08-898-300-49	Sequence 49, Appl
77	45	55.6	16	2	US-08-824-513-49	Sequence 49, Appl
78	45	55.6	125	2	US-09-248-796A-24231	
						Sequence 24231, A
79	45	55.6	150	2	US-09-395-689-2	Sequence 2, Appli
80	45	55.6	718	2	US-09-328-352-5094	Sequence 5094, Ap
81	44.5	54.9	16	2	US-09-437-912-8	Sequence 8, Appli
82	44	54.3	10	2	US-09-615-153-19	Sequence 19, Appl
83	44	54.3	16	2		
					US-10-104-307-17	Sequence 17, Appl
84	44	54.3	353	2	US-09-270-767-32624	Sequence 32624, A
85	44	54.3	353	2	US-09-270-767-47841	Sequence 47841, A
86	44	54.3	944	2	US-09-449-285A-2	Sequence 2, Appli
87	44	54.3	944	2	US-09-964-238-2	Sequence 2, Appli
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00	44	54.3	1104	2	US-10-104-047-2506	Sequence 2506, Ap

89	44	54.3	1125	2	US-09-949-016-10194	Sequence 10194, A
90	44	54.3	1214	2	US-09-949-016-6885	Sequence 6885, Ap
91	44	54.3	1318	2	US-09-949-016-7130	Sequence 7130, Ap
92	43.5	53.7	10	2	US-09-615-153-20	Sequence 20, Appl
93	43.5	53.7	219	2	US-09-270-767-57647	Sequence 57647, A
94	43.5	53.7	408	2	US-09-270-767-42361	Sequence 42361, A
95	43	53.1	111	2	US-09-902-540-12498	Sequence 12498, A
96	43	53.1	439	2	US-09-248-796A-15955	Sequence 15955, A
97	43	53.1	455	2	US-09-252-991A-24911	Sequence 24911, A
98	43	53.1	459	2	US-09-252-991A-32433	Sequence 32433, A
99	43	53.1	650	2	US-09-252-991A-19052	Sequence 19052, A
100	43	53.1	1024	2	US-10-449-315-2	Sequence 2, Appli

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03 ; Search time 55.7716 Seconds

(without alignments)

107.972 Million cell updates/sec

Title: US-10-018-103B-1

Perfect score: 81

Sequence: 1 KHKHKHKGKHKHK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published\_Applications\_AA Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A PUBCOMB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	Match	Length		ID	Description
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2	81	100.0	13	4	US-10-131-909A-1	Sequence 1, Appli
3	81	100.0	15	4	US-10-018-103A-2	Sequence 2, Appli
4	81	100.0	15	4	US-10-131-909A-2	Sequence 2, Appli
5	81	100.0	19	4	US-10-018-103A-3	Sequence 3, Appli
6	81	100.0	19	4	US-10-131-909A-3	Sequence 3, Appli
7	81	100.0	19	4	US-10-136-187-45	Sequence 45, Appl
8	81	100.0	19	5	US-10-850-873-45	Sequence 45, Appl
9	81	100.0	21	4	US-10-018-103A-9	Sequence 9, Appli
10	81	100.0	21	4	US-10-018-103A-16	Sequence 16, Appl
11	81	100.0	21	4	US-10-131-909A-9	Sequence 9, Appli
12	81	100.0	21	4	US-10-131-909A-16	Sequence 16, Appl
13	81	100.0	29	4	US-10-018-103A-4	Sequence 4, Appli
14	81	100.0	29	4	US-10-131-909A-4	Sequence 4, Appli
15	75	92.6	980	4	US-10-369-493-1406	Sequence 1406, Ap
16	75	92.6	980	4	US-10-451-467A-32	Sequence 32, Appl
17	73	90.1	29	4	US-10-018-103A-7	Sequence 7, Appli
18	73	90.1	29	4	US-10-131-909A-7	Sequence 7, Appli
19	68	84.0	1199	4	US-10-147-268-4	Sequence 4, Appli
20	68	84.0	1199	4	US-10-338-279-4	Sequence 4, Appli
21	68	84.0	1199	4	US-10-408-765A-2020	Sequence 2020, Ap
22	68	84.0	1199	5	US-10-756-149-5165	Sequence 5165, Ap

23	63	77.8	11	5	US-10-857-435A-31	Seguence	31, Appl	
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					US-09-778-200-27		27, Appl	
25	61	75.3	16	4	US-10-192-832-30		30, Appl	
26	61	75.3	16	5	US-10-431-000B-25		25, Appl	
27	61	75.3	16	5	US-10-877-068-27	=	27, Appl	
28	61	75.3	16	5	US-10-968-790-27	Sequence	27, Appl	
29	60	74.1	19	4	US-10-018-103A-13	Sequence	13, Appl	
30	60	74.1	19	4	US-10-131-909A-13		13, Appl	
31	59	72.8	1007	4	US-10-211-133-7		7, Appli	
32	59	72.8	1043	4	US-10-097-340-258	_	258, App	
33	59	72.8	_	-				
			1043	6	US-11-050-926-258		258, App	
34	58	71.6	337	4	US-10-270-333-96	_	96, Appl	
35	58	71.6	337	6	US-11-097-143-17679	_	17679, A	
36	57	70.4	104	.4	US-10-437-963-114806	Sequence	114806,	
37	56.5	69.8	874	6	US-11-097-143-18096	Sequence	18096, A	
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39	55.5	68.5	931	4	US-10-170-385-39	_	39, Appl	
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42	55	67.9	10	4 .	US-10-131-909A-14	_	14, Appl	
43	55	67.9	10	4	US-10-104-307-18		18, Appl	
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52	53	65.4	366	4	US-10-406-686A-76		76, Appl	
53	51.5	63.6	109	5	US-10-637-313-8	Sequence	8, Appli	
54	51.5	63.6	109	5	US-10-637-313-48	Sequence	48, Appl	
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56	51.5	63.6	243	5	US-10-637-313-12		12, Appl	
57	51.5	63.6	243	5	US-10-637-313-50		50, Appl	
58	51.5	63.6	305	5	US-10-450-763-51459		51459, A	
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61	51.5	63.6	415	6	US-11-051-724-76		76, Appl	
62	51.5	63.6	579	5	US-10-893-315-101		101, App	
63	51.5	63.6	579	5	US-10-893-315-105	Sequence	105, App	
64	51.5	63.6	615	4	US-10-162-335-72	Sequence	72, Appl	
65	51.5	63.6	615	5	US-10-637-313-22	Sequence	22, Appl	
66	51.5	63.6	615	6	US-11-051-724-72		72, Appl	
67	51.5	63.6	616	5	US-10-637-313-14		14, Appl	-
68	51.5	63.6	621	5	US-10-637-313-16	-	16, Appl	
69	51.5	63.6	621	5	US-10-637-313-44	-		
70							44, Appl	
	51.5	63.6	622	5	US-10-637-313-18		18, Appl	
71	51.5	63.6	626	5	US-10-507-734-25		25, Appl	
72	51.5	63.6	644	4	US-10-162-335-74	Sequence	74, Appl	
73	51.5	63.6	644	4	US-10-162-335-84	Sequence	84, Appl	
74	51.5	63.6	644	5	US-10-637-313-2	Sequence	2, Appli	
75	51.5	63.6	644	5	US-10-637-313-4		4, Appli	
76	51.5	63.6	644	5	US-10-637-313-6		6, Appli	
77	51.5	63.6	644	5	US-10-637-313-52		52, Appl	
78	51.5	63.6	644	5	US-10-637-313-54			
79	51.5	63.6					54, Appl	
			644	5	US-10-637-313-56	_	56, Appl	·
80	51.5	63.6	644	5	US-10-637-313-58		58, Appl	
81	51.5	63.6	644	5	US-10-637-313-60	Sequence	60, Appl	•
82	51.5	63.6	644	5	US-10-637-313-62	Sequence	62, Appl	
83	51.5	63.6	644	5	US-10-637-313-64	Sequence	64, Appl	
84	51.5	63.6	644	5	US-10-637-313-66	Sequence		
85	51.5	63.6	644	5	US-10-637-313-68	Sequence		
86	51.5	63.6	644	5	US-10-637-313-70	Sequence		
87	51.5	63.6	644	5	US-10-637-313-72			
88	51.5	63.6	644	5		Sequence		
89					US-10-637-313-74	Sequence		
U J	51.5	63.6	644	5	US-10-637-313-76	Sequence	/6, Appl	

90	51.5	63.6	644	5		Sequence 1180, Ap
91	51.5	63.6	644	5	US-10-450-763-51460	Sequence 51460, A
92	51.5	63.6	644	6	US-11-051-724-74	Sequence 74, Appl
93	51.5	63.6	644	6	US-11-051-724-84	Sequence 84, Appl
94	51.5	63.6	720	5	US-10-450-763-51462	Sequence 51462, A
95	51	63.0	145	6	US-11-096-568A-29065	Sequence 29065, A
96	51	63.0	207	6	US-11-096-568A-29064	Sequence 29064, A
97	50	61.7	68	4	US-10-425-115-343636	Sequence 343636,
98	. 50	61.7	79	4	US-10-424-599-245751	Sequence 245751,
99	50	61.7	119	6	US-11-096-568A-24129	Sequence 24129, A
100	50	61.7	142	6	US-11-096-568A-24128	Sequence 24128, A

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:53:38; Search time 8.10494 Seconds

(without alignments)

105.932 Million cell updates/sec

Title: US-10-018-103B-1

Perfect score: 81

Sequence: 1 KHKHKHKGKHKHK 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

용

Maximum Match 100%

Listing first 100 summaries

Database : Published\_Applications\_AA New:\*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:\*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:\*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:\*

4: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:\*

5: /EMC\_Celerra SIDS3/ptodata/2/pubpaa/PCT NEW PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Length.	DD	ID	Dogganinti	
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1	61	75.3	16	7	US-11-254-805-49	Sequence	49, Appl
. 2	61	75.3	16	7	US-11-320-468-49	Sequence	49, Appl
3	53	65.4	18	7	US-11-254-805-34	Sequence	34, Appl
4	53	65.4	18	7	US-11-320-468-34	Sequence	34, Appl
5	53	65.4	123	7	US-11-056-355B-70006	Sequence	70006, A
6	53	65.4	123	7	US-11-056-355B-87848	Sequence	87848, A
7	53	65.4	159	7	US-11-056-355B-70005	Sequence	70005, A
8	53	65.4	159	7	US-11-056-355B-87847	Sequence	87847, A
9	53	65.4	221	7	US-11-056-355B-70004	Sequence	70004, A
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 19.6296 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-2

Perfect score: 94

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	62	66.0	18	1	US-08-293-284A-64	Sequence 64, Appl
8	62	66.0	18	2	US-08-898-300-64	Sequence 64, Appl
9	62	66.0	18	2	US-08-824-513-64	Sequence 64, Appl
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 64.3519 Seconds

(without alignments)

107.972 Million cell updates/sec

Title: US-10-018-103B-2

Perfect score: 94

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Scoring table: BLOSUM62

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Searched: 2097797 seqs, 463214858 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	94	100.0	19	4	US-10-131-909A-3	Sequence 3, Appli
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97	46	48.9	407	7	US-11-056-355B-106330	Sequence 106330,
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 24.8642 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-3

Perfect score: 120

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	80	66.7	1199	2	US-10-147-268-4	Sequence 4, Appli
5	78	65.0	18	1	US-08-346-849-64	Sequence 64, Appl
6	78	65.0	18	1	US-08-293-284A-64	Sequence 64, Appl
7	78	65.0	18	2	US-08-898-300-64	Sequence 64, Appl
8	78	65.0	18	2	US-08-824-513-64	Sequence 64, Appl
9	78	65.0	313	2	US-08-686-528A-3	Sequence 3, Appli
10	78	65.0	313	2	US-09-456-287-3	Sequence 3, Appli
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93	56	46.7	381	2	US-09-919-497-96	Sequence 96, Appl
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97	55.5	46.2	726	3	US-08-951-188A-50	Sequence 50, Appl
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 81.5123 Seconds

(without alignments)

107.972 Million cell updates/sec

Title: US-10-018-103B-3

Perfect score: 120

Sequence: 1 KHKHKHKHKKKKKHKHK 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	120	100.0	19	5	US-10-850-873-45	Sequence 45, Appl
5	120	100.0	21	4	US-10-018-103A-9	Sequence 9, Appli
6	120	100.0	21	4	US-10-018-103A-16	Sequence 16, Appl
7	120	100.0	21	4	US-10-131-909A-9	Sequence 9, Appli
8	120	100.0	21	4 ·	US-10-131-909A-16	Sequence 16, Appl
9	120	100.0	29	4	US-10-018-103A-4	Sequence 4, Appli
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13	94	78.3	15	4	US-10-018-103A-2	Sequence 2, Appli
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91	63	52.5	385	5	US-10-784-004-940	Sequence 940, App
92	63	52.5	385	6	US-11-096-568A-28232	Sequence 28232, A
93	63	52.5	395	4	US-10-424-599-254664	Sequence 254664,
94	63	52.5	408	4	US-10-377-636-2	Sequence 2, Appli
95	63	52.5	899	4	US-10-437-963-122313	Sequence 122313,
96	62.5	52.1	172	4	US-10-437-963-143267	Sequence 143267,
97	62.5	52.1	526	4	US-10-437-963-143265	Sequence 143265,
98	62.5	52.1	931	4	US-10-170-385-39	Sequence 39, Appl
99	62.5	52.1	931	4	US-10-408-765A-1585	Sequence 1585, Ap
100	62	51.7	16	4	US-10-390-472-49	Sequence 49, Appl

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:53:38 ; Search time 11.8457 Seconds

(without alignments)

105.932 Million cell updates/sec

Title: US-10-018-103B-3

Perfect score: 120

Sequence: 1 KHKHKHKHKKKKKHKHKHK 19

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 232337 segs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 78 65.0 16 7 US-11-254-805-49 Sequence	49, Appl
3 78 65.0 18 7 US-11-254-805-34 Sequence	34. Appl
4 78 65.0 18 7 US-11-320-468-34 Sequence	
5 68 56.7 165 6 US-10-953-349-28541 Sequence	
6 68 56.7 165 7 US-11-056-355B-65052 Sequence	•
7 68 56.7 227 6 US-10-953-349-28540 Sequence	28540, A
8 68 56.7 227 7 US-11-056-355B-65051 Sequence	
9 68 56.7 233 6 US-10-953-349-28539 Sequence	
10 68 56.7 233 7 US-11-056-355B-65050 Sequence	65050, A
11 67 55.8 1135 6 US-10-449-902-41295 Sequence	41295, A
12 66 55.0 220 6 US-10-449-902-48827 Sequence	
13 65.5 54.6 119 7 US-11-056-355B-13846 Sequence	13846, A
14 65.5 54.6 142 7 US-11-056-355B-13845 Sequence	13845, A
15 65.5 54.6 205 7 US-11-056-355B-13844 Sequence	13844, A
16 64 53.3 299 6 US-10-953-349-5486 Sequence	5486, Ap
17 64 53.3 300 6 US-10-953-349-5485 Sequence	
18 64 53.3 448 6 US-10-953-349-5484 Sequence	
19 63 52.5 123 7 US-11-056-355B-70006 Sequence	
20 63 52.5 123 7 US-11-056-355B-87848 Sequence	

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99	54	45.0	3711	7	US-11-063-439-261	Sequence 261, App
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 37.9506 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-4

Perfect score: 183

Sequence: 1 KHKHKHKHKKKKHKHKHKHKHKHKHK 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	114	62.3	313	2	US-09-456-287~3	Sequence 3, Appli
3	114	62.3	337	2	US-08-686-528A-2	Sequence 2, Appli
4	114	62.3	337	2	US-09-456-287-2	Sequence 2, Appli
5	104.5	57.1	1199	2	US-09-208-742-2	Sequence 2, Appli
6	104.5	57.1	1199	2	US-09-332-295-4	Sequence 4, Appli
7	104.5	57.1	1199	2	US-09-709-979-4	Sequence 4, Appli
8	104.5	57.1	1199	2	US-10-147-268-4	Sequence 4, Appli
9	92.5	50.5	224	2	US-09-902-540-12716	Sequence 12716, A
10	90	49.2	400	2	US-09-543-681A-6151	Sequence 6151, Ap
11	86	47.0	297	2	US-09-489-039A-12802	Sequence 12802, A
12	84	45.9	726	2	US-09-126-980-2	Sequence 2, Appli
13	84	45.9	726	2	US-09-476-482-2	Sequence 2, Appli
14	84	45.9	726	2	US-09-517-605-6	Sequence 6, Appli
15	83.5	45.6	213	2	US-09-248-796A-16185	Sequence 16185, A
16	83.5	45.6	300	2	US-09-395-689-1	Sequence 1, Appli
17	83.5	45.6	765	1	US-08-663-112-2	Sequence 2, Appli
18	83.5	45.6	765	2	US-09-538-092-906	Sequence 906, App
19	83.5	45.6	765	2	US-09-882-274-2	Sequence 2, Appli
20	80	43.7	94	2	US-09-612-126-10	Sequence 10, Appl
21	80	43.7	179	2	US-09-612-126-11	Sequence 11, Appl

22	80	43.7	186	2	US-09-612-126-8	Sequence 8, Appli	
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33	79.5	43.4	47	2		Sequence 4, Appli	
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56	. 74	40.4	425	2	US-09-270-767-45380	Sequence 45380, A	
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61	72	39.3	163	2	US-09-902-540-13395	Sequence 13395, A	
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79	68	37.2	117	2	US-09-513-999C-5282	Sequence 5282, Ap	
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 124.414 Seconds

(without alignments)

107.972 Million cell updates/sec

Title: US-10-018-103B-4

Perfect score: 183

Sequence: 1 KHKHKHKHKKKKHKHKHKHKHKHKHK 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

욙

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:\*

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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
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(without alignments)

105.932 Million cell updates/sec

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Listing first 100 summaries

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 26.1728 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-5

Perfect score: 136

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued\_Patents\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	89	65.4	25	2	US-09-721-154-14	Sequence 14, Appl
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6	89	65.4	203	2	US-09-270-767-50543	Sequence 50543, A
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8	86	63.2	16	2	US-10-104-307-17	Sequence 17, Appl
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 85.8025 Seconds

(without alignments)

107.972 Million cell updates/sec

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:53:38 ; Search time 12.4691 Seconds

(without alignments)

105.932 Million cell updates/sec

Title: US-10-018-103B-5

Perfect score: 136

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

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Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

용

Maximum Match 100%

Listing first 100 summaries

Database : Published\_Applications\_AA\_New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	91	66.9	3397	7	US-11-063-439-245	Sequence 245, App
5	91	66.9	3520	7	US-11-063-439-112	Sequence 112, App
6	91	66.9	3524	7	US-11-063-439-61	Sequence 61, Appl
7	91	66.9	3544	7	US-11-063-439-19	Sequence 19, Appl
8	91	66.9	3544	7	US-11-063-439-158	Sequence 158, App
9	91	66.9	3578	7	US-11-063-439-74	Sequence 74, Appl
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14	90	66.2	3517	7	US-11-063-439-8	Sequence 8, Appli
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 26.1728 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-6

Perfect score: 136

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	92	67.6	203	2	US-09-270-767-50543	Sequence 50543, A
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6	90	66.2	427	2	US-09-506-066E-8	Sequence 8, Appli
7	89	65.4	399	2	US-09-506-066E-10	Sequence 10, Appl
8	86.5	63.6	16	2	US-10-104-307-17	Sequence 17, Appl
9	86.5	63.6	485	2	US-09-949-016-6557	Sequence 6557, Ap
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 85.8025 Seconds

(without alignments)

107.972 Million cell updates/sec

Title: US-10-018-103B-6

Perfect score: 136

Sequence: 1 KKHHHKHHHKKHHHKK 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%

욯

Maximum Match 100%

Listing first 100 summaries

Database: Published Applications AA Main:\*

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*

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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	136	100.0	20	4	US-10-131-909A-6	Sequence 6, Appl	
3	110.5	81.2	17	4	US-10-131-909A-17	Sequence 17, App	1
4	98	72.1	378	4	US-10-029-386-33892	Sequence 33892,	Α
5	97	71.3	49	3	US-09-864-761-37882	Sequence 37882,	Α
6	97	71.3	52	4	US-10-243-552-985	Sequence 985, Ap	р
7	97	71.3	52	5	US-10-450-763-47452	Sequence 47452,	A
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9	97	71.3	496	6	US-11-096-568A-29371	Sequence 29371,	Α
10	97	71.3	548	6	US-11-096-568A-29370	Sequence 29370,	Α
11	97	71.3	684	6	US-11-096-568A-29369	Sequence 29369,	Α
12	96	70.6	29	4	US-10-029-386-30014	Sequence 30014,	Α
13	96	70.6	233	5	US-10-450-763-50126	Sequence 50126,	Α
14	95	69.9	67	4	US-10-424-599-144585	Sequence 144585,	
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19	94	69.1	183	5	US-10-450-763-55696	Sequence 55696,	
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100	85	62.5	625	3	US-09-853-386-63	Sequence 63, Appl
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:53:38; Search time 12.4691 Seconds

(without alignments)

105.932 Million cell updates/sec

Title: US-10-018-103B-6

Perfect score: 136

Sequence: 1 KKHHHKHHHKKHHHKK 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232337 segs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

£

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:\*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:\*

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4: /EMC\_Celerra SIDS3/ptodata/2/pubpaa/US08 NEW PUB.pep:\*

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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11 NEW PUB.pep:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
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2	97	71.3	- 548	7	US-11-056-355B-71815	Sequence 71815, A
3	97	71.3	684	7	US-11-056-355B-71814	Sequence 71814, A
4	96	70.6	407	7	US-11-056-355B-106330	Sequence 106330,
5	96	70.6	407	7	US-11-056-355B-117569	Sequence 117569,
6	94	69.1	498	6	US-10-449-902-36716	Sequence 36716, A
7	94	69.1	498	6	US-10-449-902-48560	Sequence 48560, A
8	94	69.1	498	6	US-10-449-902-55170	Sequence 55170, A
9	94	69.1	3397	7	US-11-063-439-245	Sequence 245, App
10	94	69.1	3520	7	US-11-063-439-112	Sequence 112, App
11	94	69.1	3524	7	US-11-063-439-61	Sequence 61, Appl
12	94	69.1	3544	7	US-11-063-439-19	Sequence 19, Appl
13	94	69.1	3544	7	US-11-063-439-158	Sequence 158, App
14	94	69.1	3578	7	US-11-063-439-74	Sequence 74, Appl
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16	92	67.6	3496	7	US-11-063-439-230	Sequence 230, App
17	92	67.6	3517	7	US-11-063-439-8	Sequence 8, Appli
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 13.0864 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-14

Perfect score: 65

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 42.9012 Seconds

(without alignments)

107.972 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 2097797

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Maximum Match 100%

Listing first 100 summaries

Database : Published\_Applications\_AA\_Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	65	100.0	10	4	US-10-018-103A-14	Sequence 14, Appl
2	65	100.0	10	4	US-10-131-909A-14	Sequence 14, Appl
3	65	100.0	10	4	US-10-104-307-18	Sequence 18, Appl
4	65	100.0	11	5	US-10-857-435A-31	Sequence 31, Appl
5	65	100.0	29	4	US-10-018-103A-7	Sequence 7, Appli
6	65	100.0	29	4	US-10-131-909A-7	Sequence 7, Appli
7	65	100.0	104	4	US-10-437-963-114806	Sequence 114806,
8	65	100.0	1199	4	US-10-147-268-4	Sequence 4, Appli
9	65	100.0	1199	4	US-10-338-279-4	Sequence 4, Appli
10	65	100.0	1199	4	US-10-408-765A-2020	Sequence 2020, Ap
11	65	100.0	1199	5	US-10-756-149-5165	Sequence 5165, Ap
12	62	95.4	1219	6	US-11-097-143-14646	Sequence 14646, A
13	61	93.8	337	4	US-10-270-333-96	Sequence 96, Appl
14	61	93.8	337	6	US-11-097-143-17679	Sequence 17679, A
15	57	87.7	16	3	US-09-778-200-27	Sequence 27, Appl
16	57	87.7	16	4	US-10-192-832-30	Sequence 30, Appl
17	57	87.7	16	5	US-10-431-000B-25	Sequence 25, Appl
18	57	87.7	16	5	US-10-877-068-27	Sequence 27, Appl
19	57	87.7	16	5	US-10-968-790-27	Sequence 27, Appl
20	57	87.7	19	4	US-10-018-103A-3	Sequence 3, Appli
21	57	87.7	19	4	US-10-131-909A-3	Sequence 3, Appli
22	57	87.7	19	4	US-10-136-187-45	Sequence 45, Appl

23	57	87.7	19	5	US-10-850-873-45	Sequence 45, Appl
24	57	87.7	21	4	US-10-018-103A-9	Sequence 9, Appli
25	. 57	87.7	21	4	US-10-018-103A-16	Sequence 16, Appl
26	57	87.7	21	4	US-10-131-909A-9	Sequence 9, Appli
27	57	87.7	21	4	US-10-131-909A-16	Sequence 16, Appl
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29	57	87.7	29	4	US-10-131-909A-4	Sequence 4, Appli
30	57	87.7	980	4	US-10-369-493-1406	Sequence 1406, Ap
31	57	87.7	980	4	US-10-451-467A-32	Sequence 32, Appl
32	57	87.7	1007	4	US-10-211-133-7	Sequence 7, Appli
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54	49	75.4	14	3	US-09-780-933-17	Sequence 17, Appl
55	49	75.4	14	3	US-09-997-623-44	Sequence 44, Appl
56	49	75.4	14	3	US-09-978-917A-44	Sequence 44, Appl
57	49	75.4	14	3.	US-09-904-196B-12	Sequence 12, Appl
58	49	75.4	14	3	US-09-782-587B-15	
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61	49	75.4	14	4	US-10-192-294-12	Sequence 12, Appl
62	49	75.4	14	4	US-10-195-707B-38	Sequence 38, Appl
63	49	75.4	14	4	US-10-318-966-12	Sequence 12, Appl
64	49	75.4	14	4	US-10-190-414-19	Sequence 19, Appl
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76	49	75.4	14	5	US-10-950-747-15	Sequence 15, Appl
77	49	75.4	14	5	US-10-498-665-75	Sequence 75, Appl
78	49	75.4	14	6	US-11-004-111-44	Sequence 44, Appl
79	49	75.4	14	6	US-11-004-461-12	Sequence 12, Appl
80	49	75.4	14	6	US-11-053-228-12	Sequence 12, Appl
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82	49	75.4	14	_	US-11-158-848-38	
83				6		Sequence 38, Appl
	49	75.4	14	6	US-11-202-516-24	Sequence 24, Appl
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86	49	75.4	15	3	US-09-780-933-18	Sequence 18, Appl
87	49	75.4	15	3	US-09-997-623-45	Sequence 45, Appl
88	49	75.4	15	3	US-09-978-917A-45	Sequence 45, Appl
89	49	75.4	15	3	US-09-904-196B-5	Sequence 5, Appli
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90 91	49 49	75.4 75.4	15 15	3 4	US-09-782-587B-16 US-10-003-496-13	Sequence 16, Appl
		-		-		Sequence 13, Appl
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97	49	75.4	15	5	US-10-950-747-16	Sequence 16, Appl
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:53:38; Search time 6.23457 Seconds

(without alignments)

105.932 Million cell updates/sec

Title: US-10-018-103B-14

Perfect score: 65

Sequence: 1 KHKHKHKHKH 10

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	51	78.5	18	7	US-11-320-468-34	Sequence	34, Appl
5	47	72.3	113	7	US-11-056-355B-24797	Sequence	24797, A
6	47	72.3	343	6	US-10-478-743B-4	Sequence	4, Appli
7	47	72.3	359	7	US-11-056-355B-44655	Sequence	44655, A
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9	47	72.3	368	7	US-11-056-355B-30759	Sequence	30759, A
10	47	72.3	368	7	US-11-056-355B-34349	Sequence	34349, A
11	47	72.3	368	7	US-11-056-355B-41231	Sequence	41231, A
12	47	72.3	368	7	US-11-056-355B-86298	Sequence	86298, A
13	47	72.3	375	7	US-11-056-355B-44654	Sequence	44654, A
14	47	72.3	375	7	US-11-056-355B-70456	Sequence	70456, A
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17	47	72.3	381	7	US-11-056-355B-97742	Sequence	97742, A
18	47	72.3	381	7	US-11-056-355B-108981	Sequence	108981,
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53	43	66.2	16	7	US-11-320-468-29	Sequence 29, Appl
54	43	66.2	16	7	US-11-320-468-30	Sequence 30, Appl
55	43	66.2	226	7	US-11-293-697-4030	Sequence 4030, Ap
56	43	66.2	350	7		
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57	43	66.2	354	7	US-11-056-355B-10604	Sequence 10604, A
58	43	66.2	383	7	US-11-056-355B-10603	Sequence 10603, A
59	43	66.2	884	7	US-11-105-233-58	Sequence 58, Appl
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61	42	64.6	116	6	US-10-953-349-14295	Sequence 14295, A
62	42	64.6	119	7	US-11-056-355B-13846	Sequence 13846, A
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66	42	64.6	155	7	US-11-056-355B-13137	Sequence 13137, A
67	42	64.6	165	6	US-10-953-349-28541	Sequence 28541, A
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69	42	64.6	205	7	US-11-056-355B-13844	Sequence 13844, A
70	42	64.6	218	7	US-11-056-355B-13136	Sequence 13136, A
71	42	64.6	220	6	US-10-449-902-46772	Sequence 46772, A
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74	42	64.6	227	7	US-11-056-355B-65051	Sequence 65051, A
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92	41	63.1	233	6	US-10-449-902-51445	Sequence 51445, A
93	41	63.1	233	6	US-10-374-780A-488	Sequence 488, App
94	41	63.1	268	6	US-10-449-902-50912	Sequence 50912, A
95	41	63.1	293	7	US-11-056-355B-22617	Sequence 22617, A
96	41	63.1	295	7	US-11-056-355B-22616	Sequence 22616, A
97	41	63.1	307	6	US-10-196-749-262	Sequence 262, App
98	41	63.1	334	7	US-11-251-208-489	Sequence 489, App
99	41	63.1	425	6	US-10-449-902-36008	Sequence 36008, A
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:04:27; Search time 19.6296 Seconds

(without alignments)

66.887 Million cell updates/sec

Title: US-10-018-103B-15

Perfect score: 105

Sequence: 1 HHKHHKHHKHHK 15

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Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H COMB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					COLUMNICADO	
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No.	Score	Match	Length	DB	ID	Description
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2	78	74.3	79	2	US-09-248-796A-27876	Sequence 27876, A
3	78	74.3	362	2	US-09-248-796A-16633	Sequence 16633, A
4	78	74.3	399	2	US-09-506-066E-10	Sequence 10, Appl
5	77	73.3	363	2	US-09-328-352-4930	Sequence 4930, Ap
6	. 77	73.3	626	2	US-09-949-016-6776	Sequence 6776, Ap
7	77	73.3	697	2	US-09-949-016-9660	Sequence 9660, Ap
8	76	72.4	203	2	US-09-270-767-35326	Sequence 35326, A
9	76	72.4	203	2	US-09-270-767-50543	Sequence 50543, A
10	75	71.4	25	2	US-09-721-154-14	Sequence 14, Appl
11	74	70.5	16	2	US-10-104-307-17	Sequence 17, Appl
12	73	69.5	148	2	US-09-461-325-453	Sequence 453, App
13	73	69.5	148	2	US-10-012-542-453	Sequence 453, App
14	73	69.5	148	2	US-10-115-123-453	Sequence 453, App
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97	63	60.0	115	3	US-09-989-293A-95	Sequence	95,	Appl
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 64.3519 Seconds

(without alignments)

107.972 Million cell updates/sec

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Perfect score: 105

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Scoring table: BLOSUM62

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Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Maximum Match 100%

Listing first 100 summaries

Database: Published Applications AA Main:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	105	100.0	26	4	US-10-018-103A-8	Sequence 8, Appli
6	105	100.0	26	4	US-10-131-909A-8	Sequence 8, Appli
7	85	81.0	238	4	US-10-425-114-41573	Sequence 41573, A
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10	80	76.2	142	6	US-11-097-143-10002	Sequence 10002, A
11	80	76.2	227	· 5	US-10-450-763-44758	Sequence 44758, A
12	79	75.2	49	3	US-09-864-761-37882	Sequence 37882, A
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14	79	75.2	87	3	US-09-864-761-33727	Sequence 33727, A
15	79	75.2	87	3	US-09-864-761-34744	Sequence 34744, A
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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:53:38; Search time 9.35185 Seconds

(without alignments)

105.932 Million cell updates/sec

Title: US-10-018-103B-15

Perfect score: 105

Sequence: 1 HHKHHKHHKHHKH 15

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Gapop 10.0, Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Maximum Match 100%

Listing first 100 summaries

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6	77	73.3	626	7	US-11-283-329-126	Sequence 126, App
7	77	73.3	637	7	US-11-283-329-130	Sequence 130, App
8	77	73.3	684	7	US-11-056-355B-71814	Sequence 71814, A
9	77	73.3	3397	7	US-11-063-439-245	Sequence 245, App
10	77	73.3	3520	7	US-11-063-439-112	Sequence 112, App
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12	77	73.3	3544	7	US-11-063-439-19	Sequence 19, Appl
13	77	73.3	3544	7	US-11-063-439-158	Sequence 158, App
14	77	73.3	3578	7	US-11-063-439-74	Sequence 74, Appl
15	76	72.4	3482	7	US-11-063-439-48	Sequence 48, Appl
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OM protein - protein search, using sw model

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(without alignments)

66.887 Million cell updates/sec

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Listing first 100 summaries

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:52:03; Search time 90.0926 Seconds

(without alignments)

107.972 Million cell updates/sec

Title: US-10-018-103B-16

Perfect score: 130

Sequence: 1 KKHKHKHKHKKKKK 21

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:\*

1: /EMC\_Celerra SIDS3/ptodata/2/pubpaa/US07 PUBCOMB.pep:\*

2: /EMC Celerra SIDS3/ptodata/2/pubpaa/US08 PUBCOMB.pep:\*

3: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 PUBCOMB.pep:\*

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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11 PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	130	100.0	21	4	US-10-018-103A-16	Sequence 16, Appl
3	130	100.0	21	4	US-10-131-909A-9	Sequence 9, Appli
4	130	100.0	21	4	US-10-131-909A-16	Sequence 16, Appl
5	120	92.3	19	4	US-10-018-103A-3	Sequence 3, Appli
6	120	92.3	19	4	US-10-131-909A-3	Sequence 3, Appli
7	120	92.3	19	4	US-10-136-187-45	Sequence 45, Appl
8	120	92.3	19	5	US-10-850-873-45	Sequence 45, Appl
9	120	92.3	29	4	US-10-018-103A-4	Sequence 4, Appli
10	120	92.3	29	4	US-10-131-909A-4	Sequence 4, Appli
11	101	77.7	29	4	US-10-018-103A-7	Sequence 7, Appli
12	101	77.7	29	4	US-10-131-909A-7	Sequence 7, Appli
13	94.5	72.7	1007	4	US-10-211-133-7	Sequence 7, Appli
14	94.5	72.7	1043	4	US-10-097-340-258	Sequence 258, App
15	94.5	72.7	1043	6	US-11-050-926-258	Sequence 258, App
16	94	72.3	15	4	US-10-018-103A-2	Sequence 2, Appli
17	94	72.3	15	4	US-10-131-909A-2	Sequence 2, Appli
18	93	71.5	980	4	US-10-369-493-1406	Sequence 1406, Ap
19	93	71.5	980	4	US-10-451-467A-32	Sequence 32, Appl
20	90	69.2	19	4	US-10-018-103A-13	Sequence 13, Appl
21	90	69.2	19	4	US-10-131-909A-13	Sequence 13, Appl
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100	64.5	49.6	109	5	US-10-637-313-48	Sequence 48, Appl

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OM protein - protein search, using sw model

Run on: July 26, 2006, 12:53:38; Search time 13.0926 Seconds

(without alignments)

105.932 Million cell updates/sec

Title: US-10-018-103B-16

Perfect score: 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 232337 seqs, 66044171 residues

Total number of hits satisfying chosen parameters: 232337

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA New:\*

1: /EMC Celerra SIDS3/ptodata/2/pubpaa/US09 NEW PUB.pep:\*

2: /EMC\_Celerra SIDS3/ptodata/2/pubpaa/US06 NEW PUB.pep:\*

3: /EMC\_Celerra SIDS3/ptodata/2/pubpaa/US07 NEW PUB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	78	60.0	18	7	US-11-320-468-34	Sequence 3	
5	73	56.2	165	6	US-10-953-349-28541	Sequence 2	
6	73	56.2	165	7	US-11-056-355B-65052	Sequence 6	•
7	73	56.2	227	6	US-10-953-349-28540	Sequence 2	
8	73	56.2	227	7	US-11-056-355B-65051	Sequence 6	5051, A
9	73	56.2	233	6	US-10-953-349-28539	Sequence 2	8539, A
10	73	56.2	233	7	US-11-056-355B-65050	Sequence 6	5050, A
11	72	55.4	220	6	US-10-449-902-48827	Sequence 4	8827, A
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13	70.5	54.2	142	7	US-11-056-355B-13845	Sequence 1	3845, A
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17	68	52.3	144	7	US-11-056-355B-13138	Sequence 1	3138, A
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94	55	42.3	410	7	US-11-056-355B-101815	Sequence	101815,
95	55	42.3	410	7	US-11-056-355B-113054	Sequence	113054,
96	55	42.3	614	7	US-11-056-355B-45875	Sequence	45875, A
97	54.5	41.9	264	7	US-11-056-355B-73386	Sequence	73386, A
98	54.5	41.9	275	7	US-11-056-355B-30606	Sequence	30606, A
99	54.5	41.9	275	7	US-11-056-355B-34196	Sequence	34196, A
100	54.5	41.9	275	7	US-11-056-355B-76341	Sequence	76341, A